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1645
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BIOTECHNOLOGY
SYSTEMS
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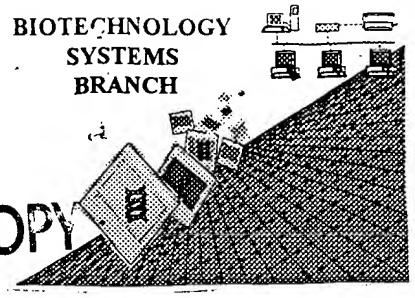

RAW SEQUENCE LISTING ERROR REPORT

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The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

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Application Serial Number: 09/647,309

Source: OIPE

Date Processed by STIC: 12/6/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
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OIPE

RAW SEQUENCE LISTING DATE: 12/06/2001
PATENT APPLICATION: US/09/647,309 TIME: 11:26:48

Input Set : A:\es.txt
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Does Not Comply
Corrected Diskette Needed
pp 1-12

RECEIVED
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TECH CENTER 1600/2900

OK

3 <110> APPLICANT: Pierre Fabre Medicament
5 <120> TITLE OF INVENTION: USE OF ACTIVE P40 CONJUGATES FOR NASAL DELIVERY
7 <130> FILE REFERENCE: D17064
9 **<140> CURRENT APPLICATION NUMBER: US/09/647,309**
10 **<141> CURRENT FILING DATE: 2001-11-30**
12 <150> PRIOR APPLICATION NUMBER: FR 98 03814
13 <151> PRIOR FILING DATE: 1998-03-27
15 <160> NUMBER OF SEQ ID NOS: 136
17 <170> SOFTWARE: PatentIn Vers. 2.0

ERRORED SEQUENCES

19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1032
E--> 21 **<212> TYPE: ADN** DNA (see 1.823 of Sequence Rules)
22 <213> ORGANISM: Klebsiella pneumoniae
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (1)..(1032)
27 <223> OTHER INFORMATION: rP40
29 <400> SEQUENCE: 1

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Met Lys Ala Ile Phe Val Leu Asn Ala Ala Pro Lys Asp Asn Thr Trp
 1               5                  10                  15

tat gca ggt ggt aaa ctg ggt tgg tcc cag tat cac gac acc ggt ttc   96
Tyr Ala Gly Gly Lys Leu Gly Trp Ser Gln Tyr His Asp Thr Gly Phe
            20                  25                  30

tac ggt aac ggt ttc cag aac aac aac ggt ccg acc cgt aac gat cag   144
Tyr Gly Asn Gly Phe Gln Asn Asn Asn Gly Pro Thr Arg Asn Asp Gln
        35                  40                  45

ctt ggt gct ggt gcg ttc ggt ggt tac cag gtt aac ccg tac ctc ggt   192
Leu Gly Ala Gly Ala Phe Gly Gly Tyr Gln Val Asn Pro Tyr Leu Gly
    50                  55                  60

ttc gaa atg ggt tat gac tgg ctg ggc cgt atg gca tat aaa ggc agc   240
Phe Glu Met Gly Tyr Asp Trp Leu Gly Arg Met Ala Tyr Lys Gly Ser
65                  70                  75                  80

gtt gac aac ggt gct ttc aaa gct cag ggc gtt cag ctg acc gct aaa   288
Val Asp Asn Gly Ala Phe Lys Ala Gln Gly Val Gln Leu Thr Ala Lys
                85                  90                  95

ctg ggt tac ccg atc act gac gat ctg gac atc tac acc cgt ctg ggc   336
Leu Gly Tyr Pro Ile Thr Asp Asp Leu Asp Ile Tyr Thr Arg Leu Gly
            100                 105                 110

ggc atg gtt tgg cgc gct gac tcc aaa ggc aac tac gct tct acc ggc   384
Gly Met Val Trp Arg Ala Asp Ser Lys Gly Asn Tyr Ala Ser Thr Gly
        115                 120                 125

gtt tcc cgt agc gaa cac gac act ggc gtt tcc cca gta ttt gct ggc   432
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RAW SEQUENCE LISTING DATE: 12/06/2001
PATENT APPLICATION: US/09/647,309 TIME: 11:26:48

Input Set : A:\es.txt
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```
 63 Val Ser Arg Ser Glu His Asp Thr Gly Val Ser Pro Val Phe Ala Gly
 64     130                 135                 140
 66 ggc gta gag tgg gct gtt act cgt gac atc gct acc cgt ctg gaa tac   480
 67 Gly Val Glu Trp Ala Val Thr Arg Asp Ile Ala Thr Arg Leu Glu Tyr
 68 145                 150                 155                 160
 70 cag tgg gtt aac aac atc ggc gac gcg ggc act gtg ggt acc cgt cct   528
 71 Gln Trp Val Asn Asn Ile Gly Asp Ala Gly Thr Val Gly Thr Arg Pro
 72                 165                 170                 175
 74 gat aac ggc atg ctg agc ctg ggc gtt tcc tac cgc ttc ggt cag gaa   576
 75 Asp Asn Gly Met Leu Ser Leu Gly Val Ser Tyr Arg Phe Gly Gln Glu
 76             180                 185                 190
 78 gat gct gca ccg gtt gtt gct ccg gct ccg gct ccg gct ccg gaa gtg   624
 79 Asp Ala Ala Pro Val Val Ala Pro Ala Pro Ala Pro Ala Pro Glu Val
 80         195                 200                 205
 82 gct acc aag cac ttc acc ctg aag tct gac gtt ctg ttc aac ttc aac   672
 83 Ala Thr Lys His Phe Thr Leu Lys Ser Asp Val Leu Phe Asn Phe Asn
 84     210                 215                 220
 86 aaa gct acc ctg aaa ccg gaa ggt cag cag gct ctg gat cag ctg tac   720
 87 Lys Ala Thr Leu Lys Pro Glu Gly Gln Gln Ala Leu Asp Gln Leu Tyr
 88 225                 230                 235                 240
 90 act cag ctg agc aac atg gat ccg aaa gac ggt tcc gct gtt gtt ctg   768
 91 Thr Gln Leu Ser Asn Met Asp Pro Lys Asp Gly Ser Ala Val Val Leu
 92                 245                 250                 255
 94 ggc tac acc gac cgc atc ggt tcc gaa gct tac aac cag cag ctg tct   816
 95 Gly Tyr Thr Asp Arg Ile Gly Ser Glu Ala Tyr Asn Gln Gln Leu Ser
 96             260                 265                 270
 98 gag aaa cgt gct cag tcc gtc gtt gac tac ctg gtt gct aaa ggc atc   864
 99 Glu Lys Arg Ala Gln Ser Val Val Asp Tyr Leu Val Ala Lys Gly Ile
100         275                 280                 285
102 ccg gct ggc aaa atc tcc gct cgc ggc atg ggt gaa tcc aac ccg gtt   912
103 Pro Ala Gly Lys Ile Ser Ala Arg Gly Met Gly Glu Ser Asn Pro Val
104     290                 295                 300
106 act ggc aac acc tgt gac aac gtg aaa gct cgc gct gcc ctg atc gat   960
107 Thr Gly Asn Thr Cys Asp Asn Val Lys Ala Arg Ala Ala Leu Ile Asp
108 305                 310                 315                 320
110 tgc ctg gct ccg gat cgt cgt gta gag atc gaa gtt aaa ggc tac aaa  1008
111 Cys Leu Ala Pro Asp Arg Arg Val Glu Ile Glu Val Lys Gly Tyr Lys
112                 325                 330                 335
114 gaa gtt gta act cag cct cag gct                               1032
115 Glu Val Val Thr Gln Pro Gln Ala
116             340
192 <210> SEQ ID NO: 3
193 <211> LENGTH: 303
E--> 194 <212> TYPE: ADN
195 <213> ORGANISM: Respiratory Syncytial Virus (RSV)
197 <220> FEATURE:
198 <221> NAME/KEY: CDS
199 <222> LOCATION: (1)..(303)
201 <220> FEATURE:
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RAW SEQUENCE LISTING DATE: 12/06/2001
PATENT APPLICATION: **US/09/647,309** TIME: 11:26:48

Input Set : **A:\es.txt**
Output Set: **N:\CRF3\12062001\I647309.raw**

```
202 <223> OTHER INFORMATION: G2A
204 <400> SEQUENCE: 3
205 acc gtg aaa acc aaa aac acc acg acc acc cag acc cag ccg agc aaa   48
206 Thr Val Lys Thr Lys Asn Thr Thr Thr Thr Gln Thr Gln Pro Ser Lys
207   1               5                  10                  15
209 ccg acc acc aaa cag cgt cag aac aaa ccg ccg aac aaa ccg aac aac   96
210 Pro Thr Thr Lys Gln Arg Gln Asn Lys Pro Pro Asn Lys Pro Asn Asn
211              20                  25                  30
213 gat ttc cat ttc gaa gtg ttc aac ttc gtg ccg tgc agc atc tgc agc   144
214 Asp Phe His Phe Glu Val Phe Asn Phe Val Pro Cys Ser Ile Cys Ser
215          35                  40                  45
217 aac aac ccg acc tgc tgg gcg atc tgc aaa cgt atc ccg aac aaa aaa   192
218 Asn Asn Pro Thr Cys Trp Ala Ile Cys Lys Arg Ile Pro Asn Lys Lys
219      50                  55                  60
221 ccg ggc aaa aaa acc acg acc aaa ccg acc aaa aaa ccg acc ttc aaa   240
222 Pro Gly Lys Lys Thr Thr Thr Lys Pro Thr Lys Lys Pro Thr Phe Lys
223  65                  70                  75                  80
225 acc acc aaa aaa gat cat aaa ccg cag acc acc aaa ccg aaa gaa gtg   288
226 Thr Thr Lys Lys Asp His Lys Pro Gln Thr Thr Lys Pro Lys Glu Val
227                  85                  90                  95
229 ccg acc acc aaa ccg                                           303
230 Pro Thr Thr Lys Pro
231              100
262 <210> SEQ ID NO: 5
263 <211> LENGTH: 303
E--> 264 <212> TYPE: ADN
265 <213> ORGANISM: Respiratory Syncytial Virus (RSV)
267 <220> FEATURE:
268 <221> NAME/KEY: CDS
269 <222> LOCATION: (1)..(303)
271 <220> FEATURE:
272 <223> OTHER INFORMATION: G2B
274 <400> SEQUENCE: 5
275 acc gcg cag acc aaa ggc cgt atc acc acc agc acc cag acc aac aaa   48
276 Thr Ala Gln Thr Lys Gly Arg Ile Thr Thr Ser Thr Gln Thr Asn Lys
277   1               5                  10                  15
279 ccg agc acc aaa agc cgt agc aaa aac ccg ccg aaa aaa ccg aaa gat   96
280 Pro Ser Thr Lys Ser Arg Ser Lys Asn Pro Pro Lys Lys Pro Lys Asp
281              20                  25                  30
283 gat tac cac ttc gaa gtg ttc aac ttc gtg ccc tgc agc atc tgc ggc   144
284 Asp Tyr His Phe Glu Val Phe Asn Phe Val Pro Cys Ser Ile Cys Gly
285          35                  40                  45
287 aac aac cag ctg tgc aaa agc atc tgc aaa acc atc ccg agc aac aaa   192
288 Asn Asn Gln Leu Cys Lys Ser Ile Cys Lys Thr Ile Pro Ser Asn Lys
289      50                  55                  60
291 ccg aaa aag aaa ccg acc atc aaa ccg acc aac aaa ccg acc acc aaa   240
292 Pro Lys Lys Lys Pro Thr Ile Lys Pro Thr Asn Lys Pro Thr Thr Lys
293  65                  70                  75                  80
295 acc acc aac aaa cgt gat ccg aaa acc ccg gcg aaa atg ccg aag aag   288
```

RAW SEQUENCE LISTING DATE: 12/06/2001
PATENT APPLICATION: US/09/647,309 TIME: 11:26:48

Input Set : A:\es.txt
Output Set: N:\CRF3\12062001\I647309.raw

```
296 Thr Thr Asn Lys Arg Asp Pro Lys Thr Pro Ala Lys Met Pro Lys Lys
297                  85                  90                  95
299 gaa atc atc acc aac                                              303
300 Glu Ile Ile Thr Asn
301             100
332 <210> SEQ ID NO: 7
333 <211> LENGTH: 303
E--> 334 <212> TYPE: ADN
335 <213> ORGANISM: Respiratory Syncytial Virus (RSV)
337 <220> FEATURE:
338 <221> NAME/KEY: CDS
339 <222> LOCATION: (1)..(303)
341 <220> FEATURE:
342 <223> OTHER INFORMATION: G2AdCys
345 <400> SEQUENCE: 7
346 acc gtg aaa acc aaa aac acc acg acc acc cag acc cag ccg agc aaa   48
347 Thr Val Lys Thr Lys Asn Thr Thr Thr Thr Gln Thr Gln Pro Ser Lys
348   1               5                  10                  15
350 ccg acc acc aaa cag cgt cag aac aaa ccg ccg aac aaa ccg aac aac   96
351 Pro Thr Thr Lys Gln Arg Gln Asn Lys Pro Pro Asn Lys Pro Asn Asn
352             20                  25                  30
354 gat ttc cat ttc gaa gtg ttc aac ttc gtg ccg agc agc atc tgc agc   144
355 Asp Phe His Phe Glu Val Phe Asn Phe Val Pro Ser Ser Ile Cys Ser
356         35                  40                  45
358 aac aac ccg acc tgc tgg gcg atc agc aaa cgt atc ccg aac aaa aaa   192
359 Asn Asn Pro Thr Cys Trp Ala Ile Ser Lys Arg Ile Pro Asn Lys Lys
360     50                  55                  60
362 ccg ggc aaa aaa acc acg acc aaa ccg acc aaa aaa ccg acc ttc aaa   240
363 Pro Gly Lys Lys Thr Thr Thr Lys Pro Thr Lys Lys Pro Thr Phe Lys
364 65                  70                  75                  80
366 acc acc aaa aaa gat cat aaa ccg cag acc acc aaa ccg aaa gaa gtg   288
367 Thr Thr Lys Lys Asp His Lys Pro Gln Thr Thr Lys Pro Lys Glu Val
368                 85                  90                  95
370 ccg acc acc aaa ccg                                              303
371 Pro Thr Thr Lys Pro
372             100
403 <210> SEQ ID NO: 9
404 <211> LENGTH: 303
E--> 405 <212> TYPE: ADN
406 <213> ORGANISM: Respiratory Syncytial Virus (RSV)
408 <220> FEATURE:
409 <221> NAME/KEY: CDS
410 <222> LOCATION: (1)..(303)
412 <220> FEATURE:
413 <223> OTHER INFORMATION: G2BdCys
416 <400> SEQUENCE: 9
417 acc gcg cag acc aaa ggc cgt atc acc acc agc acc cag acc aac aaa   48
418 Thr Ala Gln Thr Lys Gly Arg Ile Thr Thr Ser Thr Gln Thr Asn Lys
419   1               5                  10                  15
```

RAW SEQUENCE LISTING DATE: 12/06/2001
PATENT APPLICATION: US/09/647,309 TIME: 11:26:48

Input Set : A:\es.txt
Output Set: N:\CRF3\12062001\I647309.raw

```
421 ccg agc acc aaa agc cgt agc aaa aac ccg ccg aaa aaa ccg aaa gat   96
422 Pro Ser Thr Lys Ser Arg Ser Lys Asn Pro Pro Lys Lys Pro Lys Asp
423             20                  25                  30
425 gat tac cac ttc gaa gtg ttc aac ttc gtg ccc agc agc atc tgc ggc  144
426 Asp Tyr His Phe Glu Val Phe Asn Phe Val Pro Ser Ser Ile Cys Gly
427          35                  40                  45
429 aac aac cag ctg tgc aaa agc atc agc aaa acc atc ccg agc aac aaa  192
430 Asn Asn Gln Leu Cys Lys Ser Ile Ser Lys Thr Ile Pro Ser Asn Lys
431      50                  55                  60
433 ccg aaa aag aaa ccg acc atc aaa ccg acc aac aaa ccg acc acc aaa  240
434 Pro Lys Lys Lys Pro Thr Ile Lys Pro Thr Asn Lys Pro Thr Thr Lys
435  65                  70                  75                  80
437 acc acc aac aaa cgt gat ccg aaa acc ccg gcg aaa atg ccg aag aag  288
438 Thr Thr Asn Lys Arg Asp Pro Lys Thr Pro Ala Lys Met Pro Lys Lys
439                 85                  90                  95
441 gaa atc atc acc aac                                          303
442 Glu Ile Ile Thr Asn
443             100
474 <210> SEQ ID NO: 11
475 <211> LENGTH: 42
E--> 476 <212> TYPE: ADN
477 <213> ORGANISM: Respiratory Syncytial Virus (RSV)
479 <220> FEATURE:
480 <221> NAME/KEY: CDS
481 <222> LOCATION: (1)..(42)
483 <220> FEATURE:
484 <223> OTHER INFORMATION: G1ACys
487 <400> SEQUENCE: 11
488 agc atc tgc agc aac aac ccg acc tgc tgg gcg atc tgc aaa          42
489 Ser Ile Cys Ser Asn Asn Pro Thr Cys Trp Ala Ile Cys Lys
490   1               5                  10
503 <210> SEQ ID NO: 13
504 <211> LENGTH: 42
E--> 505 <212> TYPE: ADN
506 <213> ORGANISM: Respiratory Syncytial Virus (RSV)
508 <220> FEATURE:
509 <221> NAME/KEY: CDS
510 <222> LOCATION: (1)..(42)
512 <220> FEATURE:
513 <223> OTHER INFORMATION: G1BCys
517 <400> SEQUENCE: 13
518 agc atc tgc ggc aac aac cag ctg tgc aaa agc atc tgc aaa          42
519 Ser Ile Cys Gly Asn Asn Gln Leu Cys Lys Ser Ile Cys Lys
520   1               5                  10
533 <210> SEQ ID NO: 15
534 <211> LENGTH: 42
E--> 535 <212> TYPE: ADN
536 <213> ORGANISM: Respiratory Syncytial Virus (RSV)
538 <220> FEATURE:
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RAW SEQUENCE LISTING DATE: 12/06/2001
PATENT APPLICATION: US/09/647,309 TIME: 11:26:48

Input Set : A:\es.txt
Output Set: N:\CRF3\12062001\I647309.raw

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539 <221> NAME/KEY: CDS
540 <222> LOCATION: (1)..(42)
542 <220> FEATURE:
543 <223> OTHER INFORMATION: G1A
546 <400> SEQUENCE: 15
547 agc atc tgc agc aac aac ccg acc tgc tgg gcg atc agc aaa          42
548 Ser Ile Cys Ser Asn Asn Pro Thr Cys Trp Ala Ile Ser Lys
549   1               5                  10
562 <210> SEQ ID NO: 17
563 <211> LENGTH: 42
E--> 564 <212> TYPE: ADN
565 <213> ORGANISM: Respiratory Syncytial Virus (RSV)
567 <220> FEATURE:
568 <221> NAME/KEY: CDS
569 <222> LOCATION: (1)..(42)
571 <220> FEATURE:
572 <223> OTHER INFORMATION: G1B
575 <400> SEQUENCE: 17
576 agc atc tgc ggc aac aac cag ctg tgc aaa agc atc agc aaa          42
577 Ser Ile Cys Gly Asn Asn Gln Leu Cys Lys Ser Ile Ser Lys
578   1               5                  10
659 <210> SEQ ID NO: 23
660 <211> LENGTH: 303
E--> 661 <212> TYPE: ADN
662 <213> ORGANISM: Respiratory Syncytial Virus (RSV)
664 <220> FEATURE:
665 <221> NAME/KEY: CDS
666 <222> LOCATION: (1)..(303)
668 <220> FEATURE:
669 <223> OTHER INFORMATION: G2AdCF
672 <400> SEQUENCE: 23
673 acc gtg aaa acc aaa aac acc acg acc acc cag acc cag ccg agc aaa   48
674 Thr Val Lys Thr Lys Asn Thr Thr Thr Thr Gln Thr Gln Pro Ser Lys
675   1               5                  10                  15
677 ccg acc acc aaa cag cgt cag aac aaa ccg ccg aac aaa ccg aac aac   96
678 Pro Thr Thr Lys Gln Arg Gln Asn Lys Pro Pro Asn Lys Pro Asn Asn
679              20                  25                  30
681 gat tcc cat tcc gaa gtg tcc aac tcc gtg ccg agc agc atc tgc agc   144
682 Asp Ser His Ser Glu Val Ser Asn Ser Val Pro Ser Ser Ile Cys Ser
683          35                  40                  45
685 aac aac ccg acc tgc tgg gcg atc agc aaa cgt atc ccg aac aaa aaa   192
686 Asn Asn Pro Thr Cys Trp Ala Ile Ser Lys Arg Ile Pro Asn Lys Lys
687      50                  55                  60
689 ccg ggc aaa aaa acc acg acc aaa ccg acc aaa aaa ccg acc ttc aaa   240
690 Pro Gly Lys Lys Thr Thr Thr Lys Pro Thr Lys Lys Pro Thr Phe Lys
691  65                  70                  75                  80
693 acc acc aaa aaa gat cat aaa ccg cag acc acc aaa ccg aaa gaa gtg   288
694 Thr Thr Lys Lys Asp His Lys Pro Gln Thr Thr Lys Pro Lys Glu Val
695                 85                  90                  95
```

RAW SEQUENCE LISTING DATE: 12/06/2001
PATENT APPLICATION: US/09/647,309 TIME: 11:26:48

Input Set : A:\es.txt
Output Set: N:\CRF3\12062001\I647309.raw

```
     697 ccg acc acc aaa ccg                                                303
     698 Pro Thr Thr Lys Pro
     699             100
     730 <210> SEQ ID NO: 25
     731 <211> LENGTH: 51
E--> 732 <212> TYPE: ADN
     733 <213> ORGANISM: Respiratory Syncytial Virus (RSV)
     735 <220> FEATURE:
     736 <221> NAME/KEY: CDS
     737 <222> LOCATION: (1)..(51)
     739 <220> FEATURE:
     740 <223> OTHER INFORMATION: G4A
     742 <400> SEQUENCE: 25
     743 gtg ccg tgc agc atc tgc agc aac aac ccg acc tgc tgg gcg atc tgc   48
     744 Val Pro Cys Ser Ile Cys Ser Asn Asn Pro Thr Cys Trp Ala Ile Cys
     745   1               5                  10                  15
     747 aaa                                                            51
     748 Lys
     764 <210> SEQ ID NO: 27
     765 <211> LENGTH: 51
E--> 766 <212> TYPE: ADN
     767 <213> ORGANISM: Respiratory Syncytial Virus (RSV)
     769 <220> FEATURE:
     770 <221> NAME/KEY: CDS
     771 <222> LOCATION: (1)..(51)
     773 <220> FEATURE:
     774 <223> OTHER INFORMATION: G4AdC
     777 <400> SEQUENCE: 27
     778 gtg ccg agc agc atc tgc agc aac aac ccg acc tgc tgg gcg atc agc   48
     779 Val Pro Ser Ser Ile Cys Ser Asn Asn Pro Thr Cys Trp Ala Ile Ser
     780   1               5                  10                  15
     782 aaa                                                            51
     783 Lys
     799 <210> SEQ ID NO: 29
     800 <211> LENGTH: 51
E--> 801 <212> TYPE: ADN
     802 <213> ORGANISM: Respiratory Syncytial Virus (RSV)
     804 <220> FEATURE:
     805 <221> NAME/KEY: CDS
     806 <222> LOCATION: (1)..(51)
     808 <220> FEATURE:
     809 <223> OTHER INFORMATION: G4B
     812 <400> SEQUENCE: 29
     813 gtg ccc tgc agc atc tgc ggc aac aac cag ctg tgc aaa agc atc tgc   48
     814 Val Pro Cys Ser Ile Cys Gly Asn Asn Gln Leu Cys Lys Ser Ile Cys
     815   1               5                  10                  15
     817 aaa                                                            51
     818 Lys
     834 <210> SEQ ID NO: 31
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RAW SEQUENCE LISTING DATE: 12/06/2001
PATENT APPLICATION: US/09/647,309 TIME: 11:26:48

Input Set : A:\es.txt
Output Set: N:\CRF3\12062001\I647309.raw

```
     835 <211> LENGTH: 51
E--> 836 <212> TYPE: ADN
     837 <213> ORGANISM: Respiratory syncytial Virus (RSV)
     839 <220> FEATURE:
     840 <221> NAME/KEY: CDS
     841 <222> LOCATION: (1)..(51)
     843 <220> FEATURE:
     844 <223> OTHER INFORMATION: G4BdC
     847 <400> SEQUENCE: 31
     848 gtg ccc agc agc atc tgc ggc aac aac cag ctg tgc aaa agc atc agc   48
     849 Val Pro Ser Ser Ile Cys Gly Asn Asn Gln Leu Cys Lys Ser Ile Ser
     850   1               5                  10                  15
     852 aaa                                                           51
     853 Lys
     949 <210> SEQ ID NO: 37
     950 <211> LENGTH: 183
E--> 951 <212> TYPE: ADN
     952 <213> ORGANISM: Respiratory syncytial Virus (RSV)
     954 <220> FEATURE:
     955 <221> NAME/KEY: CDS
     956 <222> LOCATION: (1)..(183)
     958 <220> FEATURE:
     959 <223> OTHER INFORMATION: G200A
     962 <400> SEQUENCE: 37
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     964 Gln Thr Gln Pro Ser Lys Pro Thr Thr Lys Gln Arg Gln Asn Lys Pro
     965   1               5                  10                  15
     967 ccg aac aaa ccg aac aac gat ttc cat ttc gaa gtg ttc aac ttc gtg   96
     968 Pro Asn Lys Pro Asn Asn Asp Phe His Phe Glu Val Phe Asn Phe Val
     969              20                  25                  30
     971 ccg tgc agc atc tgc agc aac aac ccg acc tgc tgg gcg atc tgc aaa   144
     972 Pro Cys Ser Ile Cys Ser Asn Asn Pro Thr Cys Trp Ala Ile Cys Lys
     973          35                  40                  45
     975 cgt atc ccg aac aaa aaa ccg ggc aaa aaa acc acg acc               183
     976 Arg Ile Pro Asn Lys Lys Pro Gly Lys Lys Thr Thr Thr
     977      50                  55                  60
     999 <210> SEQ ID NO: 39
    1000 <211> LENGTH: 177
E--> 1001 <212> TYPE: ADN
    1002 <213> ORGANISM: Respiratory syncytial Virus (RSV)
    1004 <220> FEATURE:
    1005 <221> NAME/KEY: CDS
    1006 <222> LOCATION: (1)..(177)
    1008 <220> FEATURE:
    1009 <223> OTHER INFORMATION: G198A
    1012 <400> SEQUENCE: 39
    1013 cag acc cag ccg agc aaa ccg acc acc aaa cag cgt cag aac aaa ccg   48
    1014 Gln Thr Gln Pro Ser Lys Pro Thr Thr Lys Gln Arg Gln Asn Lys Pro
    1015   1               5                  10                  15
```

RAW SEQUENCE LISTING DATE: 12/06/2001
PATENT APPLICATION: US/09/647,309 TIME: 11:26:48

Input Set : A:\es.txt
Output Set: N:\CRF3\12062001\I647309.raw

```
1017 ccg aac aaa ccg aac aac gat ttc cat ttc gaa gtg ttc aac ttc gtg   96
1018 Pro Asn Lys Pro Asn Asn Asp Phe His Phe Glu Val Phe Asn Phe Val
1019             20                  25                  30
1021 ccg tgc agc atc tgc agc aac aac ccg acc tgc tgg gcg atc tgc aaa   144
1022 Pro Cys Ser Ile Cys Ser Asn Asn Pro Thr Cys Trp Ala Ile Cys Lys
1023          35                  40                  45
1025 cgt atc ccg aac aaa aaa ccg ggc aaa aaa acc                       177
1026 Arg Ile Pro Asn Lys Lys Pro Gly Lys Lys Thr
1027      50                  55
1049 <210> SEQ ID NO: 41
1050 <211> LENGTH: 171
E--> 1051 <212> TYPE: ADN
1052 <213> ORGANISM: Respiratory syncytial Virus (RSV)
1054 <220> FEATURE:
1055 <221> NAME/KEY: CDS
1056 <222> LOCATION: (1)..(171)
1058 <220> FEATURE:
1059 <223> OTHER INFORMATION: G196A
1062 <400> SEQUENCE: 41
1063 cag acc cag ccg agc aaa ccg acc acc aaa cag cgt cag aac aaa ccg   48
1064 Gln Thr Gln Pro Ser Lys Pro Thr Thr Lys Gln Arg Gln Asn Lys Pro
1065   1               5                  10                  15
1067 ccg aac aaa ccg aac aac gat ttc cat ttc gaa gtg ttc aac ttc gtg   96
1068 Pro Asn Lys Pro Asn Asn Asp Phe His Phe Glu Val Phe Asn Phe Val
1069             20                  25                  30
1071 ccg tgc agc atc tgc agc aac aac ccg acc tgc tgg gcg atc tgc aaa   144
1072 Pro Cys Ser Ile Cys Ser Asn Asn Pro Thr Cys Trp Ala Ile Cys Lys
1073          35                  40                  45
1075 cgt atc ccg aac aaa aaa ccg ggc aaa                               171
1076 Arg Ile Pro Asn Lys Lys Pro Gly Lys
1077      50                  55
1099 <210> SEQ ID NO: 43
1100 <211> LENGTH: 165
E--> 1101 <212> TYPE: ADN
1102 <213> ORGANISM: Respiratory syncytial Virus (RSV)
1104 <220> FEATURE:
1105 <221> NAME/KEY: CDS
1106 <222> LOCATION: (1)..(165)
1108 <220> FEATURE:
1109 <223> OTHER INFORMATION: G194A
1112 <400> SEQUENCE: 43
1113 cag acc cag ccg agc aaa ccg acc acc aaa cag cgt cag aac aaa ccg   48
1114 Gln Thr Gln Pro Ser Lys Pro Thr Thr Lys Gln Arg Gln Asn Lys Pro
1115   1               5                  10                  15
1117 ccg aac aaa ccg aac aac gat ttc cat ttc gaa gtg ttc aac ttc gtg   96
1118 Pro Asn Lys Pro Asn Asn Asp Phe His Phe Glu Val Phe Asn Phe Val
1119             20                  25                  30
1121 ccg tgc agc atc tgc agc aac aac ccg acc tgc tgg gcg atc tgc aaa   144
1122 Pro Cys Ser Ile Cys Ser Asn Asn Pro Thr Cys Trp Ala Ile Cys Lys
```

RAW SEQUENCE LISTING DATE: 12/06/2001
PATENT APPLICATION: US/09/647,309 TIME: 11:26:48

Input Set : A:\es.txt
Output Set: N:\CRF3\12062001\I647309.raw

```
1123          35                  40                  45
1125 cgt atc ccg aac aaa aaa ccg                                    165
1126 Arg Ile Pro Asn Lys Lys Pro
1127      50                  55
1149 <210> SEQ ID NO: 45
1150 <211> LENGTH: 159
E--> 1151 <212> TYPE: ADN
1152 <213> ORGANISM: Respiratory syncytial Virus (RSV)
1154 <220> FEATURE:
1155 <221> NAME/KEY: CDS
1156 <222> LOCATION: (1)..(159)
1158 <220> FEATURE:
1159 <223> OTHER INFORMATION: G192A
1162 <400> SEQUENCE: 45
1163 cag acc cag ccg agc aaa ccg acc acc aaa cag cgt cag aac aaa ccg   48
1164 Gln Thr Gln Pro Ser Lys Pro Thr Thr Lys Gln Arg Gln Asn Lys Pro
1165   1               5                  10                  15
1167 ccg aac aaa ccg aac aac gat ttc cat ttc gaa gtg ttc aac ttc gtg   96
1168 Pro Asn Lys Pro Asn Asn Asp Phe His Phe Glu Val Phe Asn Phe Val
1169              20                  25                  30
1171 ccg tgc agc atc tgc agc aac aac ccg acc tgc tgg gcg atc tgc aaa   144
1172 Pro Cys Ser Ile Cys Ser Asn Asn Pro Thr Cys Trp Ala Ile Cys Lys
1173          35                  40                  45
1175 cgt atc ccg aac aaa                                            159
1176 Arg Ile Pro Asn Lys
1177      50
1199 <210> SEQ ID NO: 47
1200 <211> LENGTH: 153
E--> 1201 <212> TYPE: ADN
1202 <213> ORGANISM: Respiratory syncytial Virus (RSV)
1204 <220> FEATURE:
1205 <221> NAME/KEY: CDS
1206 <222> LOCATION: (1)..(153)
1208 <220> FEATURE:
1209 <223> OTHER INFORMATION: G6A
1212 <400> SEQUENCE: 47
1213 cag acc cag ccg agc aaa ccg acc acc aaa cag cgt cag aac aaa ccg   48
1214 Gln Thr Gln Pro Ser Lys Pro Thr Thr Lys Gln Arg Gln Asn Lys Pro
1215   1               5                  10                  15
1217 ccg aac aaa ccg aac aac gat ttc cat ttc gaa gtg ttc aac ttc gtg   96
1218 Pro Asn Lys Pro Asn Asn Asp Phe His Phe Glu Val Phe Asn Phe Val
1219              20                  25                  30
1221 ccg tgc agc atc tgc agc aac aac ccg acc tgc tgg gcg atc tgc aaa   144
1222 Pro Cys Ser Ile Cys Ser Asn Asn Pro Thr Cys Trp Ala Ile Cys Lys
1223          35                  40                  45
1225 cgt atc ccg                                                    153
1226 Arg Ile Pro
1227      50
3327 <210> SEQ ID NO: 136
```

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RAW SEQUENCE LISTING DATE: 12/06/2001
PATENT APPLICATION: US/09/647,309 TIME: 11:26:49

Input Set : A:\es.txt
Output Set: N:\CRF3\12062001\I647309.raw

3328 <211> LENGTH: 15
3329 <212> TYPE: PRT
3330 <213> ORGANISM: Respiratory syncytial Virus (RSV)
3332 <220> FEATURE:
3333 <223> OTHER INFORMATION: Xaa means orn.
3335 <220> FEATURE:
3336 <223> OTHER INFORMATION: G1'
3339 <400> SEQUENCE: 136
W--> 3340 Ser Ile Asp Ser Asn Asn Pro Thr Xaa Trp Ala Ile Ser Lys Cys
3341 1 5 10 15
E--> 3345 1
E--> 3348 -16-
E--> 3349 PF82PCTSEQ/dln

delete

see next page

<210> 79
<211> 183
<212> ADN
<213> Respiratory syncytial Virus (RSV)

<220>
<221> CDS
<222> (1)..(183)

<220> G200BdC move down - <220> never has a response
<223>

FYI Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY DATE: 12/06/2001
PATENT APPLICATION: US/09/647,309 TIME: 11:26:50

Input Set : A:\es.txt
Output Set: N:\CRF3\12062001\I647309.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:21 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:194 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:264 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:334 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:405 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:476 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:505 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:535 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:564 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:604 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:19
L:604 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:19
L:604 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:621 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:20
L:621 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:20
L:621 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:638 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21
L:638 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21
L:638 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:655 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:22
L:655 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
L:655 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:661 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:732 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:766 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:801 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:836 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:882 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:33
L:882 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:33
L:882 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:902 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:34
L:902 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:34
L:902 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:922 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:35
L:922 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:35
L:922 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:942 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:36
L:942 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:36
L:942 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36
L:951 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1001 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1051 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1101 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1151 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1201 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1251 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1293 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:

VERIFICATION SUMMARY DATE: 12/06/2001
PATENT APPLICATION: US/09/647,309 TIME: 11:26:50

Input Set : A:\es.txt
Output Set: N:\CRF3\12062001\I647309.raw

L:1342 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1392 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1442 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1491 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1541 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1591 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1633 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1683 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1733 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1783 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1833 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1883 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1933 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1975 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1982 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:2025 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:2075 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:2125 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:2175 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:2225 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:2275 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:2325 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:2367 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:2438 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:2509 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:2559 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:2609 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:2659 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:2709 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:3224 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:129
L:3224 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:129
L:3224 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:129
L:3244 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:130
L:3244 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:130
L:3244 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:130
L:3323 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:135
L:3323 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:135
L:3323 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:135
L:3340 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:136
L:3340 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:136
L:3340 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:136
L:3345 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:136
M:332 Repeated in SeqNo=136
L:3349 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:3349 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:3349 M:252 E: No. of Seq. differs, <211>LENGTH:Input:15 Found:16 SEQ:136